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☐ 1: Q96PY6. Serine/threonine-...[gi:22256934]

BLink, Domains, Links

LOCUS Q96PY6 1258 aa linear PRI 15-SEP-2003
 DEFINITION Serine/threonine-protein kinase Nek1 (NimA-related protein kinase 1) (NY-REN-55 antigen).

ACCESSION Q96PY6
 VERSION Q96PY6 GI:22256934
 DBSOURCE swissprot: locus NEK1_HUMAN, accession Q96PY6;
 class: standard.
 extra accessions: Q9Y594, created: Feb 28, 2003.
 sequence updated: Feb 28, 2003.
 annotation updated: Sep 15, 2003.

xrefs: gi: [15620860](#), gi: [15620861](#), gi: [5360120](#), gi: [5360121](#)
 xrefs (non-sequence databases): GenewHGNC:7744, MIM [604588](#),
 InterProIPR000719, InterProIPR008271, InterProIPR002290,
 InterProIPR001245, PfamPF00069, PRINTSPR00109, ProDomPD000001,
 SMARTSM00220, PROSITEPS00107, PROSITEPS50011, PROSITEPS00108
 KEYWORDS Serine/threonine-protein kinase; ATP-binding; Mitosis;
 Nuclear protein; Phosphorylation; Cell cycle; Cell division;
 Tyrosine-protein kinase; Alternative splicing.

SOURCE Homo sapiens (human)
 ORGANISM *Homo sapiens*
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 1258)
 AUTHORS Nagase, T., Kikuno, R. and Ohara, O.
 TITLE Prediction of the coding sequences of unidentified human genes.
 XXI. The complete sequences of 60 new cDNA clones from brain which
 code for large proteins

JOURNAL DNA Res. 8 (4), 179-187 (2001)
 MEDLINE [21456161](#)
 PUBMED [11572484](#)
 REMARK SEQUENCE FROM N.A. (ISOFORM 1).
 TISSUE=Brain

REFERENCE 2 (residues 1 to 1258)
 AUTHORS Scanlan, M.J., Gordan, J.D., Williamson, B., Stockert, E., Bander, N.H.,
 Jongeneel, C.V., Gure, A.O., Jager, D., Jager, E., Knuth, A., Chen, Y.-T.
 and Old, L.J.

TITLE Antigens recognized by autologous antibody in patients with
 renal-cell carcinoma
 JOURNAL Int. J. Cancer 83 (4), 456-464 (1999)
 MEDLINE [99438124](#)
 PUBMED [10508479](#)
 REMARK SEQUENCE OF 444-1258 FROM N.A. (ISOFORM 2).
 TISSUE=Renal cell carcinoma

COMMENT -----
 This SWISS-PROT entry is copyright. It is produced through a
 collaboration between the Swiss Institute of Bioinformatics and
 the EMBL outstation - the European Bioinformatics Institute.

The original entry is available from <http://www.expasy.ch/sprot> and <http://www.ebi.ac.uk/sprot>

[FUNCTION] PHOSPHORYLATES SERINES AND THREONINES, BUT ALSO APPEARS TO POSSESS TYROSINE KINASE ACTIVITY. IMPLICATED IN THE CONTROL OF MEIOSIS (By similarity).
 [CATALYTIC ACTIVITY] ATP + a protein = ADP + a phosphoprotein.
 [SUBCELLULAR LOCATION] Nuclear (Probable).
 [ALTERNATIVE PRODUCTS] Event=Alternative splicing; Named isoforms=2; Name=1; IsoId=Q96PY6-1; Sequence=Displayed; Name=2; IsoId=Q96PY6-2; Sequence=VSP_004870; Note=No experimental confirmation available.
 [SIMILARITY] Belongs to the Ser/Thr family of protein kinases. NIMA subfamily.

FEATURES	Location/Qualifiers
<u>source</u>	1..1258 /organism="Homo sapiens" /db_xref="taxon:9606"
<u>gene</u>	1..1258 /gene="NEK1" /note="synonym: KIAA1901"
<u>Protein</u>	1..1258 /gene="NEK1" /product="Serine/threonine-protein kinase Nek1" /EC_number="2.7.1.37"
<u>Region</u>	4..258 /gene="NEK1" /region_name="Domain" /note="PROTEIN KINASE."
<u>Site</u>	10..18 /gene="NEK1" /site_type="np-binding" /note="ATP (BY SIMILARITY)."
<u>Site</u>	33 /gene="NEK1" /site_type="binding" /note="ATP (BY SIMILARITY)."
<u>Site</u>	128 /gene="NEK1" /site_type="active" /note="BY SIMILARITY."
<u>Site</u>	162 /gene="NEK1" /site_type="phosphorylation" /note="(AUTO-) (BY SIMILARITY)."
<u>Region</u>	478..521 /gene="NEK1" /region_name="Splicing variant" /note="Missing (in isoform 2). /FTId=VSP_004870."
<u>Region</u>	1232 /gene="NEK1" /region_name="Conflict" /note="G -> E (IN REF. 2)."

ORIGIN

```

1 mekyvrlqki gegsfkgail vkstedgrgy vikeinism sskereesr evavlannkh
61 pnivqyresf eengslyivm dyceggdlfk rinaqkgvlf qedqlldwfv qiclalknhv
121 drkilhrdik sqnifltdkg tvqlgdfiga rvlnstvela rtcigtpyyl speicenkpy
181 nnksdiwalg cvlyelctlk hafeagsmkn lvkiisgsf ppvslhysyd lrsllvsqflk
241 rnrdprsvn silekgfiak riekflspql iaefclktf skfgsqpipa krpasgqnsi
301 svmpaqkitk paakygipla ykkygdcklh ekplqkhkq ahqtpekrvn tgeerrkise

```

361 eaarkrrlef ieekkkqkdq iislmkaegm krgekerler inrareggwr nvlslaggsge
421 vkapflgsgg tiapssfssr ggyehyhaif dqmqggraed neakwkreyi grglpergil
481 pgvrpgfpyg aaghhfhpda ddirktlkrl kavskqanan rkggqlaver akqveeflqr
541 kreamqnkar aeghmvyarl lrqirlqnf erqqikaklr gekkeanhse gqegseeadm
601 rrkkieslka hanaraavlk eqlerkrkea yerekkvwee hlvakgvkss dvspplgqhe
661 tggspskqgm rvisvtsal kevgvdsst dtretseemg ktnnaisskr eilrrlnenl
721 kaqedekgkq nlsdtfeinv hedakeheke ksvssdrkkw eaggqlvipl deltdtsfs
781 tterhtvgev iklgpnspr rawgksptds vlkilgeael qlqtellent tirseispeg
841 ekykplitge kkvcqishei npsaivdspv etkspefsea spqmslkleg nleppddlet
901 eilgepsgt n kdeslpctit dwwiseeket ketgsadrit iqenevsedg vstvdqlsd
961 ihiepgtnds qhskcdvdks vqpepfhkv vhsehlnlvp qvgsvcqspe esfafrshsh
1021 lppknknkns lliglstglf dannpkmlrt clspdlsklf rtlmdvptvg dvrqdnleid
1081 eiedenikeg psdsedivfe etdtdlqelq asmeqlrlreg pgeeyseeee svlknsvdpe
1141 tangtdvade ddnpsasal neewhdsnd geiasececd svfnhleelr lhlegemgfe
1201 kffevyekik aihededeni eicskivqni lgnehqhlya kilhlvmadg ayqednde

//

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Oct 14 2003 07:44:30

Comparison between SEQ ID NO:4 and Q96PY6

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAUTa4Xs: 1214 aa
>seqid4
vs /tmp/fastaDAAVTa4Xs library
searching /tmp/fastaDAAVTa4Xs library

1258 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 40, opt: 28, gap-pen: -12/-2, width: 16
Scan time: 0.034

The best scores are:

sp|Q96PY6|NEK1_HUMAN Serine/threonine-protein kin (1258) 4775 opt

>>sp|Q96PY6|NEK1_HUMAN Serine/threonine-protein kinase N (1258 aa)
initn: 4773 initl: 4773 opt: 4775

Smith-Waterman score: 7822; 96.343% identity in 1258 aa overlap (1-1214:1-1258)

	10	20	30	40	50	60
seqid4	MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISRMSSKERESRREVAVLANKMH					
					
sp Q96	MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISRMSSKERESRREVAVLANKMH					
					
	10	20	30	40	50	60
seqid4	PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWVQICLALKHVVH					
					
sp Q96	PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWVQICLALKHVVH					
					
	70	80	90	100	110	120
seqid4	DRKILHRDIKSQNIPLTKDGTWQLGDFGIARVLNSTVELARTCIGTPPYLSPEICENKPY					
					
sp Q96	DRKILHRDIKSQNIPLTKDGTWQLGDFGIARVLNSTVELARTCIGTPPYLSPEICENKPY					
					
	130	140	150	160	170	180
seqid4	NNKSDIWLGCVLVELCTLKHAFAEAGSMKNLVLKIIISGSFPPVSLHYSYDLRSLVSQLEK					
					
sp Q96	NNKSDIWLGCVLVELCTLKHAFAEAGSMKNLVLKIIISGSFPPVSLHYSYDLRSLVSQLEK					
					
	190	200	210	220	230	240
seqid4	RNPRDRPSVNSILEKGFIAKRIEKLSPQLIAEEFCLKTFSKFGSQPIPAKRPAQSQNSI					
					
sp Q96	RNPRDRPSVNSILEKGFIAKRIEKLSPQLIAEEFCLKTFSKFGSQPIPAKRPAQSQNSI					
					
	250	260	270	280	290	300
seqid4	SVMPAQKITKPAKYGIPLAYKKYGDKKLHEKKPLQKHKQAHQTEKRVNTGEERRKISE					
					

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sp|Q96 SVPAQKITPAKYGGLPLAYKYGDKKLHEKKPLQKHKQAHQTPKEKRVNTGEERRKISE
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      .....
sp|Q96 EAARKRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQGWNRNVL SAGSGSE
      370      380      390      400      410      420
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      430      440      450      460      470      480
seqid4 -----
      .....
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      490      500      510      520      530      540
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      .....
sp|Q96 RRKIESLKAHANARA AVLKEQLERKRKKEAYEREKKVWEHLVAKGVSSDVS PPLGQHE
      610      620      630      640      650      660
seqid4 TGGSPSKQQMRSVLSVTSALKEVGVDSSLTDTRETSEEMQKTNNAISSKREILRRNLNL
      .....
sp|Q96 TGGSPSKQQMRSVLSVTSALKEVGVDSSLTDTRETSEEMQKTNNAISSKREILRRNLNL
      670      680      690      700      710      720
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      .....
sp|Q96 KAQEDEKGMQLNSDTFEINVHEDAKEHEKEKSVSDRRKKWEAGGQLVLPDELTLDTSSFS
      730      740      750      760      770      780
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      790      800      810      820      830      840
seqid4 EKYKPLITGEKKVQCISHEINPSAIVDSVPVETKSPFSEASQMSKLKLEGNLEEPDDLET
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sp|Q96 EKYKPLITGEKKVQCISHEINPSAIVDSVPVETKSPFSEASQMSKLKLEGNLEEPDDLET
      850      860      870      880      890      900
seqid4 EILQEPSGNTKNKDESLPCTITDWVISEEKETKETQADRRTIQENEVSEDGVSSVTQDLS
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sp|Q96 EILQEPSGNTKNKDESLPCTITDWVISEEKETKETQADRRTIQENEVSEDGVSSVTQDLS

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	910	920	930	940	950	960
seqid4	920	930	940	950	960	970
	IHIEPGTND	QHSKCDV	DKSVQPE	PFHKKV	VHSEHLN	LVQVQSVQCSPEESFAFRSHSH
sp Q96	IHIEPGTND	QHSKCDV	DKSVQPE	PFHKKV	VHSEHLN	LVQVQSVQCSPEESFAFRSHSH
	970	980	990	1000	1010	1020
seqid4	980	990	1000	1010	1020	1030
	LPPKNKNK	NSLLIGL	STGLFDAN	NPKMLRT	CSLPDL	SKLFRTLM
sp Q96	LPPKNKNK	NSLLIGL	STGLFDAN	NPKMLRT	CSLPDL	SKLFRTLM
	1030	1040	1050	1060	1070	1080
seqid4	1040	1050	1060	1070	1080	1090
	EIKDENIK	EGPSDSE	DIVFEET	DTDLQEL	QASMEQL	LRQPGEEYSEEEESVLKNSDVEP
sp Q96	EIKDENIK	EGPSDSE	DIVFEET	DTDLQEL	QASMEQL	LRQPGEEYSEEEESVLKNSDVEP
	1090	1100	1110	1120	1130	1140
seqid4	1100	1110	1120	1130	1140	1150
	TANGTDVA	EDDNPSS	ESALNEE	WHSDNSD	GEIASCE	CDSVFNHLEELRLHLEQEMGFE
sp Q96	TANGTDVA	EDDNPSS	ESALNEE	WHSDNSD	GEIASCE	CDSVFNHLEELRLHLEQEMGFE
	1150	1160	1170	1180	1190	1200
seqid4	1160	1170	1180	1190	1200	1210
	KFFEYVEK	IKAIHEDE	DENIEIC	SKIVQNI	LNGNEHQ	HLHYAKILHLVMADGAYQEDNDE
sp Q96	KFFEYVEK	IKAIHEDE	DENIEIC	SKIVQNI	LNGNEHQ	HLHYAKILHLVMADGAYQEDNDE
	1210	1220	1230	1240	1250	